

## SEQUENCE LISTING

&lt;110&gt; Taylor, Alexander H

<120> Monoclonal Antibodies with Reduced  
Immunogenicity

&lt;130&gt; P50770

&lt;150&gt; 60/083,367

&lt;151&gt; 1998-04-28

&lt;160&gt; 97

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 429

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(429)

&lt;400&gt; 1

atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

1

5

10

15

gtc ctg tcc cag gtg cag ttg cag gag tcg ggc cca gga ctg gtg aag 96

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys

20

25

30

cct tca cag acc ttg tcc ctg acc tgc gct gtg tct ggt ggc tcc atc 144

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile

35

40

45

act agt gct tac tac tat tgg agc tgg atc cgc cag tca cca ggg aag 192  
 Thr Ser Ala Tyr Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys

50

55

60

gga ctg gag tgg att ggg agt atc tat tat agt ggg acc att ttc tcc 240  
 Gly Leu Glu Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Thr Ile Phe Ser  
 65 70 75 80

aac cca tcc ctc aag agt cga gtc gcc atg tca gta ggc acg tcc aag 288  
 Asn Pro Ser Leu Lys Ser Arg Val Ala Met Ser Val Gly Thr Ser Lys  
 85 90 95

acc cag ttc tcc ctg agc ttg agt tct gtg acc gcc gcg gac acg gcc 336  
 Thr Gln Phe Ser Leu Ser Leu Ser Ser Val Thr Ala Ala Asp Thr Ala  
 100 105 110

gtg tac tac tgt gcg aga ggt ctg ctc ctc acc att gga ctg acc aac 384  
 Val Tyr Tyr Cys Ala Arg Gly Leu Leu Leu Thr Ile Gly Leu Thr Asn  
 115 120 125

tac tac ttt gac tac tgg ggc ccg gga acc ctg gtc acc gtc ttc 429  
 Tyr Tyr Phe Asp Tyr Trp Gly Pro Gly Thr Leu Val Thr Val Phe  
 130 135 140

&lt;210&gt; 2

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(414)

&lt;400&gt; 2

atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

gtc ctg tcc cag gtg cag cta cag gag tgg ggc cca gga cta gtg aag 96  
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys  
 20 25 30

ccg tca cag acc ctg tcc ctc acc tgc ggt gtc tct ggt gcc tcc atc 144  
 Pro Ser Gln Thr Leu Ser Leu Thr Cys Gly Val Ser Gly Ala Ser Ile  
 35 40 45

aat agt ggt gtt cat tac tgg gcc tgg ata cgc cag cct gca gga aag 192  
 Asn Ser Gly Val His Tyr Trp Ala Trp Ile Arg Gln Pro Ala Gly Lys  
 50 55 60

gga ctg gag tgg att ggc aat atc tat cat agt ggg agc gcc tac tac 240  
 Gly Leu Glu Trp Ile Gly Asn Ile Tyr His Ser Gly Ser Ala Tyr Tyr  
 65 70 75 80

act cca tcc ctc gag agt cga gtc tcc atg tca ata gag acg tcc aag 288  
 Thr Pro Ser Leu Glu Ser Arg Val Ser Met Ser Ile Glu Thr Ser Lys  
 85 90 95

agc cag ttc ttc cta aac tta aat tct ctg acc gcc gcg gac acg gct 336  
 Ser Gln Phe Phe Leu Asn Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala  
 100 105 110

atc tat tat tgt gcg aga cga cat act tgg tca gac tac ttt gac ttt 384  
 Ile Tyr Tyr Cys Ala Arg Arg His Thr Ser Ser Asp Tyr Phe Asp Phe  
 115 120 125

tgg ggc cgc gga atc ctg gtc atc gtc tcc 414  
 Trp Gly Arg Gly Ile Leu Val Ile Val Ser  
 130 135

<210> 3  
 <211> 427  
 <212> DNA  
 <213> Pan troglodytes

<220>  
 <221> CDS  
 <222> (1)...(427)

<400> 3

atg ggg tca acc gcc atc ctc gcc ctc ctc ctg gct gtt ctc gaa gga 48  
 Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Glu Gly  
 1 5 10 15

gtc cgt gca gac gtg cag ctg gtg cag tcc gga gca gag gtg aaa aag 96  
 Val Arg Ala Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

ccc ggg gag tct ctg aag atc tcc tgt aag gtc tct gga aat gaa ttt 144  
 Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Val Ser Gly Asn Glu Phe  
 35 40 45

acc aac tac tgg atc gcc tgg gtg cgc cag atg tcc ggg aaa ggc ctg 192  
 Thr Asn Tyr Trp Ile Ala Trp Val Arg Gln Met Ser Gly Lys Gly Leu  
 50 55 60

gag tgg atg ggg agc atc tat cct ggt gac tct gat acc aga tac aac 240  
 Glu Trp Met Gly Ser Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Asn  
 65 70 75 80

ccg tcc ttc caa ggc caa gtc acc ttt tca gcc gac aag tcc atc acc 288  
 Pro Ser Phe Gln Gly Gln Val Thr Phe Ser Ala Asp Lys Ser Ile Thr  
 85 90 95

acc gcc tat ttg cag tgg agt agt ctg gag gcc tcg gac acc gcc atg 336  
 Thr Ala Tyr Leu Gln Trp Ser Ser Leu Glu Ala Ser Asp Thr Ala Met  
 100 105 110

tac tac tgt gcg agc cga aat cac ttt gtt ttc ggg gaa gtt att act 384  
 Tyr Tyr Cys Ala Ser Arg Asn His Phe Val Phe Gly Glu Val Ile Thr  
 115 120 125

act ttg acg gct ggg gcc agg gaa acc ctg ggt cac cgt ctc c 427  
 Thr Leu Thr Ala Gly Ala Arg Glu Thr Leu Gly His Arg Leu  
 130 135 140

<210> 4

<211> 402

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)...(402)

<400> 4

ttg ggg ctc cgc tgg gtt ttc ctt gtt gct ttt tta gaa ggt gtc cag 48  
 Leu Gly Leu Arg Trp Val Phe Leu Val Ala Phe Leu Glu Gly Val Gln  
 1 5 10 15

tgt gag gta cag ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg 96  
 Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly  
 20 25 30

ggg tcc ttg aca ctc tcc tgt gca gcc tct gga ttc acc ttc agt agg 144  
 Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg  
 35 40 45

agt ggc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg ggg tgg 192  
 Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gly Trp  
 50 55 60

ctt gca tac att gat tat ggc agt att ttc ata tac tac tcg gac tca 240

Leu Ala Tyr Ile Asp Tyr Gly Ser Ile Phe Ile Tyr Tyr Ser Asp Ser  
 65 70 75 80

gtg aag ggc cgc ttc acc atc tcc aga gac aac gcc aag aat tca ctc 288  
 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu  
 85 90 95

tat ctg caa atg aac agc ctg aga gcc gac gac acg gct ttt tat tac 336  
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Phe Tyr Tyr  
 100 105 110

tgt acg acc cat aat tgg ggg gag tta act gac tac tgg ggc cag gga 384  
 Cys Thr Thr His Asn Trp Gly Glu Leu Thr Asp Tyr Trp Gly Gln Gly  
 115 120 125

acc ctg gtc acc gtc tcc 402  
 Thr Leu Val Thr Val Ser  
 130

<210> 5  
 <211> 408  
 <212> DNA  
 <213> Pan troglodytes

<220>  
 <221> CDS

<222> (1) ... (408)

<400> 5

atg gaa ttg ggg ctc cgc tgg gtt ttc ctt gtt gct ttt tta gaa ggt 48  
 Met Glu Leu Gly Leu Arg Trp Val Phe Leu Val Ala Phe Leu Glu Gly  
 1 5 10 15

gtc cag tgt gag gta cag ctg gtg gag tct ggg gga ggc ttg gta cag 96  
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
 20 25 30

cct ggg ggg tcc ttg aca ctc tcc tgt gca gcc tct gga ttc acc ttc 144  
 Pro Gly Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
           35                          40                          45

agt agg agt ggc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg 192  
 Ser Arg Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
           50                          55                          60

gag tgg ctt gca tac att gat tat ggc agt att ttc ata tac tac tcg 240  
 Glu Trp Leu Ala Tyr Ile Asp Tyr Gly Ser Ile Phe Ile Tyr Tyr Ser  
           65                          70                          75                          80

gac tca gtg aag ggc cgc ttc acc atc tcc aga gac aac gcc aag aat 288  
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
                                   85                                  90                                  95

tca ctc tat ctg caa atg aac agc ctg aga gcc gac gac acg gct ttt 336  
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Phe  
                           100                          105                          110

tat tac tgt acg acc cat aat tgg ggg gag tta act gac tac tgg ggc 384  
 Tyr Tyr Cys Thr Thr His Asn Trp Gly Glu Leu Thr Asp Tyr Trp Gly  
           115                          120                          125

cag gga acc ctg gtc acc gtc tcc 408  
 Gln Gly Thr Leu Val Thr Val Ser

130

135

&lt;210&gt; 6

&lt;211&gt; 421

&lt;212&gt; DNA

&lt;213&gt; Pan. troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(421)

&lt;400&gt; 6

atg atg ggg tca acc gcc atc ctc gcc ctc ctc ctg gct gtt ctc caa 48  
 Met Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln

1 5 10 15

gga gtc tgt gca gag gtg cag ctg gtg cag tct gga gca gag gtg aaa 96  
 Gly Val Cys Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys

20 25 30

aag ccc ggg gag tct ctg aag atc tcc tgt aag ggc tct gga tac agt 144  
 Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser

35 40 45

ttt acc aac tac tgg atg ggc tgg gtg tgc cag atg ccc ggg aaa ggc 192  
 Phe Thr Asn Tyr Trp Met Gly Trp Val Cys Gln Met Pro Gly Lys Gly

50 55 60

ccg gag tgc atg ggg atc atc tat cct gat gac tct gat acc aga tac 240  
 Pro Glu Cys Met Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr

65 70 75 80

agc ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc 288  
 Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile

85 90 95

agc acc gcc tac cta caa tgg agc aac ctg aag gcc tcg gac acc gcc 336  
 Ser Thr Ala Tyr Leu Gln Trp Ser Asn Leu Lys Ala Ser Asp Thr Ala

100 105 110

ata tat tac tgt gcg aga tgt tat ggt tgg act act tgc gaa gct ttt 384  
 Ile Tyr Tyr Cys Ala Arg Cys Tyr Gly Trp Thr Thr Cys Glu Ala Phe

115 120 125

gat atc tgg ggc caa ggg aca atg gtc acc gtc tct t 421  
 Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser



130

135

140

&lt;210&gt; 7

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(417)

&lt;400&gt; 7

ttg	tgg	ttc	ttc	ctt	ctc	ctg	gtg	gca	gct	ccc	aga	tgg	gtc	ctg	tcc	48
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	Val	Leu	Ser	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

1				5						10					15	
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cag	ctg	cag	ctg	cag	gag	tcg	ggc	cca	gga	ctg	gtg	aag	cct	tca	cag	96
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

Gln	Leu	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gln	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

				20						25					30	
--	--	--	--	----	--	--	--	--	--	----	--	--	--	--	----	--

acc	ctg	tcc	ctc	acc	tgc	act	gtc	tct	ggc	ggc	tcc	atc	agc	agt	ggc	144
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Gly	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

				35						40					45	
--	--	--	--	----	--	--	--	--	--	----	--	--	--	--	----	--

agt	tac	tac	tgg	agt	tgg	atc	cgg	cag	ccc	gcc	ggg	aag	cga	ctg	gag	192
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ser	Tyr	Tyr	Trp	Ser	Trp	Ile	Arg	Gln	Pro	Ala	Gly	Lys	Arg	Leu	Glu	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

50										55						60
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tgg	att	ggg	tat	att	tat	tat	agt	ggg	agt	acc	tac	tac	aac	cca	tcc	240
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Trp	Ile	Gly	Tyr	Ile	Tyr	Tyr	Ser	Gly	Ser	Thr	Tyr	Tyr	Asn	Pro	Ser	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

65										70						80
----	--	--	--	--	--	--	--	--	--	----	--	--	--	--	--	----

ctc	aag	agt	cga	gtc	acc	ata	tca	gta	gac	acg	tcc	aag	aac	cag	ttc	288
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

				85						90					95	
--	--	--	--	----	--	--	--	--	--	----	--	--	--	--	----	--

tcc ctg aag ctg agc tct gtg acc gcc gca gac acg gcc gtc tat tac 336  
 Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
 100 105 110

tgt gcg aga tct ccc caa aac gta tta caa tct ttg gac tgc ttc gac 384  
 Cys Ala Arg Ser Pro Gln Asn Val Leu Gln Ser Leu Asp Cys Phe Asp  
 115 120 125

ccc tgg ggc cag gga acc ctg gtc acc gtc tcc 417  
 Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
 130 135

<210> 8

<211> 369

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)...(369)

<400> 8

gtc cag tcc cag gtc cag ctg gtg cag tcc ggg gct gag gtg aag aag 48  
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 1 5 10 15

cct ggg tcc tca gtg aag gtc tcc tgc aag gtt tcc gga ggc acc ttc 96  
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Val Ser Gly Gly Thr Phe  
 20 25 30

agc acc tat ggt ttc agc tgg gtg cgg cag gcc cct gga caa ggg ctt 144  
 Ser Thr Tyr Gly Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 35 40 45

gag tgg atg gga atg atc atc cct atc gtt ggc aca gta aag tac gca 192  
 Glu Trp Met Gly Met Ile Ile Pro Ile Val Gly Thr Val Lys Tyr Ala

50

55

60

cag agg ttc cag ggc aga gtc tca att aat gcg gac aca tcc acg aat 240  
 Gln Arg Phe Gln Gly Arg Val Ser Ile Asn Ala Asp Thr Ser Thr Asn  
 65 70 75 80

ata gcc tac atg gag ctg acc agc ctg aga tct gag gac acg gcc gtc 288  
 Ile Ala Tyr Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val  
 85 90 95

tat tac tgt gcg aca gat ctg acg gtg act act aat gat gca ttt gat 336  
 Tyr Tyr Cys Ala Thr Asp Leu Thr Val Thr Thr Asn Asp Ala Phe Asp  
 100 105 110

atc tgg ggc caa ggg aca atg gtc acc gtc tct 369  
 Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser  
 115 120

&lt;210&gt; 9

&lt;211&gt; 423

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(423)

&lt;400&gt; 9

atg gag ttt ggg ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt 48  
 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly  
 1 5 10 15

gtc cag tgt gag gtg cag ctg gtg gag tct ggg gaa ggc ttg gta aag 96  
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Glu Gly Leu Val Lys  
 20 25 30

cct ggg ggt tcc ctg aga ctc tgc tgt gca gcc tct gga ttc acc ttc 144  
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
           35                          40                          45

~~agt agt ttt ctt atg ttc tgg gtc cgc cag gct cca gaa aag ggg ctg~~ 192  
 Ser Ser Phe Leu Met Phe Trp Val Arg Gln Ala Pro Glu Lys Gly Leu  
           50                          55                          60

gag tgg gtc tca act att gat gtt agt ggt ggt aat atg tgg tac cga 240  
 Glu Trp Val Ser Thr Ile Asp Val Ser Gly Gly Asn Met Trp Tyr Arg  
           65                          70                          75                          80

gac tct gtc aag ggc cga ttc acc atg tcc aga gac aat tcc aag aac 288  
 Asp Ser Val Lys Gly Arg Phe Thr Met Ser Arg Asp Asn Ser Lys Asn  
                                   85                          90                          95

aca ctg tat ctg caa atg acc agc ctg aga gcc gac gac acg gcc gtt 336  
 Thr Leu Tyr Leu Gln Met Thr Ser Leu Arg Ala Asp Asp Thr Ala Val  
                           100                          105                          110

tac tat tgt gcg aga gag gga cga gac cct agc ggc act tgg gga tac 384  
 Tyr Tyr Cys Ala Arg Glu Gly Arg Asp Pro Ser Gly Thr Trp Gly Tyr  
           115                          120                          125

ttt gac tac tgg ggc cag gga atc ctg gtc acc gtc tcc 423  
 Phe Asp Tyr Trp Gly Gln Gly Ile Leu Val Thr Val Ser  
           130                          135                          140

<210> 10

<211> 97

<212> PRT

<213> Pan troglodytes

<220>

<221> DOMAIN

<222> (31)...(37)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (52)...(67)

&lt;223&gt; CDRII

&lt;400&gt; 10

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Thr Ser Ala  
 20 25 30  
 Tyr Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu  
 35 40 45  
 Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Thr Ile Phe Ser Asn Pro Ser  
 50 55 60  
 Leu Lys Ser Arg Val Ala Met Ser Val Gly Thr Ser Lys Thr Gln Phe  
 65 70 75 80  
 Ser Leu Ser Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
 85 90 95  
 Cys

&lt;210&gt; 11

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(37)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (52)...(67)

&lt;223&gt; CDRII

&lt;400&gt; 11

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Gly Val Ser Gly Ala Ser Ile Asn Ser Gly  
 20 25 30  
 Val His Tyr Trp Ala Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu  
 35 40 45  
 Trp Ile Gly Asn Ile Tyr His Ser Gly Ser Ala Tyr Tyr Thr Pro Ser  
 50 55 60  
 Leu Glu Ser Arg Val Ser Met Ser Ile Glu Thr Ser Lys Ser Gln Phe  
 65 70 75 80  
 Phe Leu Asn Leu Asn Ser Leu Thr Ala Asp Thr Ala Ile Tyr Tyr Cys  
 85 90 95

<210> 12  
 <211> 96  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 12

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15  
 Ser Leu Lys Ile Ser Cys Lys Val Ser Gly Asn Glu Phe Thr Asn Tyr  
 20 25 30  
 Trp Ile Ala Trp Val Arg Gln Met Ser Gly Lys Gly Leu Glu Trp Met  
 35 40 45  
 Gly Ser Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Asn Pro Ser Phe  
 50 55 60  
 Gln Gly Gln Val Thr Phe Ser Ala Asp Lys Ser Ile Thr Thr Ala Tyr

65                      70                      75                      80  
 Leu Gln Trp Ser Ser Leu Glu Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
                          85                      90                      95

<210> 13  
 <211> 96  
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<220>  
 <221> DOMAIN  
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<221> DOMAIN  
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 <223> CDRII

<400> 13

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1                      5                      10                      15  
 Ser Leu Lys Ile Ser Cys Lys Val Ser Gly Asn Glu Phe Thr Asn Tyr  
                          20                      25                      30  
 Trp Ile Ala Trp Val Arg Gln Met Ser Gly Lys Gly Leu Glu Trp Met  
                          35                      40                      45  
 Gly Ser Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Asn Pro Ser Phe  
                          50                      55                      60  
 Gln Gly Gln Val Thr Phe Ser Ala Asp Lys Ser Ile Thr Thr Ala Tyr  
 65                      70                      75                      80  
 Leu Gln Trp Ser Ser Leu Glu Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
                          85                      90                      95

<210> 14  
 <211> 96  
 <212> PRT  
 <213> Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 14

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5						10				15	
Ser	Leu	Thr	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Ser
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Gly	Trp	Leu
		35					40					45			
Ala	Tyr	Ile	Asp	Tyr	Gly	Ser	Ile	Phe	Ile	Tyr	Tyr	Ser	Asp	Ser	Val
	50					55				60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
65					70				75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Phe	Tyr	Tyr	Cys
					85				90				95		

&lt;210&gt; 15

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII



&lt;400&gt; 15

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15  
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr  
 20 25 30  
 Trp Met Gly Trp Val Cys Gln Met Pro Gly Lys Gly Pro Glu Cys Met  
 35 40 45  
 Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60  
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80  
 Leu Gln Trp Ser Asn Leu Lys Ala Ser Asp Thr Ala Ile Tyr Tyr Cys  
 85 90 95

&lt;210&gt; 16

&lt;211&gt; 97

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(37)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (52)...(67)

&lt;223&gt; CDRII

&lt;400&gt; 16

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly  
 20 25 30  
 Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Arg Leu Glu  
 35 40 45  
 Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser  
 50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe  
 65 70 75 80  
 Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
 85 90 95  
 Cys

<210> 17  
 <211> 96  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 17

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Val Ser Gly Gly Thr Phe Ser Thr Tyr  
 20 25 30  
 Gly Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
 35 40 45  
 Gly Met Ile Ile Pro Ile Val Gly Thr Val Lys Tyr Ala Gln Arg Phe  
 50 55 60  
 Gln Gly Arg Val Ser Ile Asn Ala Asp Thr Ser Thr Asn Ile Ala Tyr  
 65 70 75 80  
 Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

<210> 18  
 <211> 96

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 18

Glu Val Gln Leu Val Glu Ser Gly Glu Gly Leu Val Lys Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe  
 20 25 30  
 Leu Met Phe Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Thr Ile Asp Val Ser Gly Gly Asn Met Trp Tyr Arg Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Met Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Thr Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

&lt;210&gt; 19

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(381)

&lt;400&gt; 19

atg agg gtc cct gct cag ctc ctg ggg ctc ctg ctc tgg ctc tca

48

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Ser  
 1 5 10 15

ggt gcc aga tgt gac atc cag atg acc cag ttt cca tcc tcc ctg tct 96  
 Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Phe Pro Ser Ser Leu Ser  
 20 25 30

gca tct gta gga gac aga gtc acc atc act tgc cag tca agt cag agc 144  
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser  
 35 40 45

att tac aac tgc ttg agt tgg tat cag cag aaa cca ggg aag gcc cct 192  
 Ile Tyr Asn Cys Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
 50 55 60

aca ctc cta atc tat ggt gca ttc acc ttg aat agt ggg gtc cca tca 240  
 Thr Leu Leu Ile Tyr Gly Ala Phe Thr Leu Asn Ser Gly Val Pro Ser  
 65 70 75 80

aga ttc agt ggc agt gga tct ggc aca gat ttc act ctc acc atc agc 288  
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
 85 90 95

aat ctg caa cct gaa gat ttt gca aca tat tac tgt cag cgt ggt tac 336  
 Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Arg Gly Tyr  
 100 105 110

ggc aca cag ctc act ttc ggt gga ggg acc aag gtg gag atc aag 381  
 Gly Thr Gln Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 115 120 125

<210> 20

<211> 384

<212> DNA

<213> Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(384)

&lt;400&gt; 20

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48  
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

ctc cca ggt acc aga tgt gac atc cag atg acc cag tct cca tcc tcc 96  
 Leu Pro Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 20 25 30

ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gcc agt 144  
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
 35 40 45

cag ggc att agc aat tat tta gcc tgg tat cag cag aaa cca ggg aaa 192  
 Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys  
 50 55 60

gcc cct aag ctc ctc atc tat tat gca tcc aga ttg gaa agt ggg gtc 240  
 Ala Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Arg Leu Glu Ser Gly Val  
 65 70 75 80

cca tca agg ttc agc ggc agt gga tct ggg acg gat tac act ctc acc 288  
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr  
 85 90 95

atc agc agc ctg cag cct gaa gat ttt gca act tat tac tgt caa cag 336  
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln  
 100 105 110

tat aac agt aac ccc ttt tcg gtg gag gga cca agg tgg aga tca aac 384  
 Tyr Asn Ser Asn Pro Phe Ser Val Glu Gly Pro Arg Trp Arg Ser Asn  
 115 120 125

&lt;210&gt; 21

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(384)

&lt;400&gt; 21

atg tcg cca tca caa ctc att ggg ttt ctg ctg ctc tgg gtt cca gcc 48

Met Ser Pro Ser Gln Leu Ile Gly Phe Leu Leu Leu Trp Val Pro Ala

1 5 10 15

tcc agg ggt gaa att gtg ctg act cag tct cca gac ttt cag tct gtg 96

Ser Arg Gly Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val

20 25 30

cct cca aag gag aaa gtc acc atc acc tgc cgg gcc agt cag agc att 144

Pro Pro Lys Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile

35 40 45

ggg agt agc tta cac tgg tac cag cag aaa cca ggt cag tct cca aag 192

Gly Ser Ser Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys

50 55 60

ctc ctc atc aag tat gct tcc cag tcc atc tca ggg gtc ccc tcg agg 240

Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Val Pro Ser Arg

65 70 75 80

ttc agt ggc agt gga tct ggg aca gat ttc acc ctc acc atc aat agc 288

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser

85 90 95

ctg gaa gct gaa gat gct gca acg tat tac tgt cag caa agt agt aat 336

Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Asn

100

105

110

tta cct cat acg ctc act ttc ggt gga ggg acc aag gtg gag atc aaa 384  
 Leu Pro His Thr Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 115 120 125

&lt;210&gt; 22

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(372)

&lt;400&gt; 22

gtc cct gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc tca ggt gcc 48  
 Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Ser Gly Ala  
 1 5 10 15

aga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct 96  
 Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser  
 20 25 30

gta gga gac aga gtc acc atc act tgc cag gca agt cag agc att agc 144  
 Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser  
 35 40 45

aac tat ttg agt tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc 192  
 Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu  
 50 55 60

ctg atc tat gat gca tcc act ttg caa agt ggg gtc cca tca agg ttc 240  
 Leu Ile Tyr Asp Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe  
 65 70 75 80

agt ggc agt gga tct ggg aca gat ttc act ctc acc atc agc agt ctg 288  
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu  
                     85                    90                    95

caa cct gaa gat ttt gca aca tat tac tgt cag cgt ggt tac ggt aca 336  
 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Arg Gly Tyr Gly Thr  
                     100                    105                    110

ctc act ttc ggt gga ggg acc aag gtg gag atc aaa 372  
 Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
                     115                    120

<210> 23  
 <211> 384  
 <212> DNA  
 <213> Pan troglodytes

<220>  
 <221> CDS  
 <222> (1)...(384)

<400> 23

atg gaa gcc cca gcg cag ctt ctc ttc ctc ctg cta ctc tgg ctc cca 48  
 Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro  
                     1                    5                    10                    15

gat acc acc gga gaa ata gtg ttg acg cag tct cca gcc acc ctg tct 96  
 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser  
                     20                    25                    30

ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt 144  
 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser  
                     35                    40                    45

gtt agc agg tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc 192  
 Val Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro



50

55

60

agg ctc ctc atc tat ggt gca tcc aac agg gcc act ggc atc cca gcc 240  
 Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala  
 65 70 75 80

agg ttc agt ggc agt ggg tct agg aca gac ttc act ctc acc atc agc 288  
 Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Ser  
 85 90 95

agc gtg gag cct gaa gat ttt gca gtt tat tac tgt cag cag tat aat 336  
 Ser Val Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn  
 100 105 110

aac cag cct ctg atc gcc ttc ggc caa ggg aca cga ctg gag att aaa 384  
 Asn Gln Pro Leu Ile Ala Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
 115 120 125

&lt;210&gt; 24

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(387)

&lt;400&gt; 24

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48  
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

ttc cca ggt gcc aaa tgt gac atc cag atg acc cag tct cct tcc acc 96  
 Phe Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Thr  
 20 25 30

ctg tct gcc tcc ata gga gac aga gtc acc atc act tgt cgg gct agt 144  
 Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
           35                          40                          45

cag ggc atc tat aat tat ttg aat tgg tat cag caa aaa cca ggg aga 192  
 Gln Gly Ile Tyr Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Arg  
           50                          55                          60

gcc cct gga ctc ctc atc ttt ggt gcc agg aat ttg gag act ggg gtc 240  
 Ala Pro Gly Leu Leu Ile Phe Gly Ala Arg Asn Leu Glu Thr Gly Val  
           65                          70                          75                          80

cca tca aca ttc agc ggc agt ggt tcc ggg aca cac ttc act ctc acc 288  
 Pro Ser Thr Phe Ser Gly Ser Gly Ser Gly Thr His Phe Thr Leu Thr  
                           85                          90                          95

atc agc agc ctg cag cct ggt gat ttt gcg act tat tac tgt cag caa 336  
 Ile Ser Ser Leu Gln Pro Gly Asp Phe Ala Thr Tyr Tyr Cys Gln Gln  
                           100                          105                          110

tat tat act acc ccg tat act ttt ggc cag ggg acc aag ctg gag atc 384  
 Tyr Tyr Thr Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile  
           115                          120                          125

aaa 387

<210> 25

<211> 387

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)...(387)

<400> 25

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctc tgt 48

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys

1 5 10 15

ttc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tcc tca 96

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser

20 25 30

ctg tct gct tct gta gga gac aga gtc acc atc tct tgt cgg gcg agt 144

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser

35 40 45

ctg gat att agc acc tgg tta gcc tgg tat cag cag aaa cca ggg aaa 192

Leu Asp Ile Ser Thr Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys

50 55 60

gcc cct aag ccc ctg atc tat gct gca tcc act ttg cca agt ggg gtc 240

Ala Pro Lys Pro Leu Ile Tyr Ala Ala Ser Thr Leu Pro Ser Gly Val

65 70 75 80

cca tcg agg ttc agc ggc agt gga tct ggg aca gat ttc act ctc acc 288

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

85 90 95

atc agc agc ctg cag cct gaa gat tct gca act tat tac tgc cga caa 336

Ile Ser Ser Leu Gln Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Arg Gln

100 105 110

tat aat agt tat ccg ctc act ttc ggt gga ggg acc aag gtg gag atc 384

Tyr Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile

115 120 125

aag 387

<210> 26

<211> 372

<212> DNA

<213> Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(372)

&lt;400&gt; 26

tct	act	cag	ctc	ctg	ggg	ctc	ctg	ctg	ctc	tgg	ctc	cca	ggg	gcc	aaa	48
Ser	Thr	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Pro	Gly	Ala	Lys	
1			5						10					15		

tgt	gac	atc	cag	atg	acc	cag	tct	cct	tcc	acc	ctg	tct	gca	tct	gta	96
Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	
			20					25					30			

gga	gac	aga	gtc	acc	atc	act	tgc	cgg	gcc	agt	cag	ggg	att	agt	agc	144
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Ser	
		35					40					45				

tgg	tta	gcc	tgg	tat	cag	cag	aaa	cca	ggg	aaa	gcc	cct	aag	ctc	ctg	192
Trp	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	
	50					55					60					

atc	tat	aag	gca	tct	agt	tta	gaa	agt	ggg	gtc	cca	tca	agg	ttc	agc	240
Ile	Tyr	Lys	Ala	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	
	65					70				75				80		

ggc	agt	gga	tct	ggg	aca	gaa	ttc	act	ctc	acc	atc	agc	agc	ctg	cag	288
Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	
			85						90					95		

cct	gat	gat	ttt	gca	act	tat	tac	tgc	caa	cag	tat	agt	agt	tac	cct	336
Pro	Asp	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Ser	Ser	Tyr	Pro	
			100					105						110		

cga	acg	ttc	ggc	caa	ggg	acc	aag	ctg	gaa	atc	aaa					372
Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys					
			115					120								

<213> Pan troglodytes

<222> (1) ... (387)

1                      5                      10                      15

20                      25                      30

35                      40                      45

50                      55                      60

65 70 75 80

85                      90                      95

55

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His

100

105

110

ggt tac ggt aca cat ccc act ttc ggt gga ggg acc aag gtg gag atc

384

Gly Tyr Gly Thr His Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile

115

120

125

aaa

387

&lt;210&gt; 28

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 28

Asp Ile Gln Met Thr Gln Phe Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser Ile Tyr Asn Cys

20

25

30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Thr Leu Leu Ile

35

40

45

Tyr Gly Ala Phe Thr Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys

85

<210> 29  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24) ... (34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50) ... (66)  
 <223> CDRII

<400> 29

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr  
 20 25 30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Tyr Ala Ser Arg Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys  
 85

<210> 30  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24) ... (34)  
 <223> CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 30

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Pro Pro Lys

1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Ser Ser

20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala

65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys

85

&lt;210&gt; 31

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 31

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Asn Tyr



20 25 30  
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Asp Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys  
 85

<210> 32  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 32

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr  
 20 25 30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
 35 40 45  
 Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Glu Pro  
 65 70 75 80  
 Glu Asp Phe Ala Val Tyr Tyr Cys  
 85

<210> 33  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 33

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Tyr Asn Tyr  
 20 25 30  
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro Gly Leu Leu Ile  
 35 40 45  
 Phe Gly Ala Arg Asn Leu Glu Thr Gly Val Pro Ser Thr Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Gly Asp Phe Ala Thr Tyr Tyr Cys

85

<210> 34  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 34

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Leu Asp Ile Ser Thr Trp  
 20 25 30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile  
 35 40 45  
 Tyr Ala Ala Ser Thr Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Ser Ala Thr Tyr Tyr Cys  
 85

&lt;210&gt; 35

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 35

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp  
                   20                                  25                                  30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
                   35                                  40                                  45  
 Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly  
                   50                                  55                                  60  
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
                   65                                  70                                  75                                  80  
 Asp Asp Phe Ala Thr Tyr Tyr Cys  
   85

<210> 36  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes  
  
 <220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI  
  
 <221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 36

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
                   1                                  5                                  10                                  15  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr  
                   20                                  25                                  30  
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
                   35                                  40                                  45  
 Tyr Tyr Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
                   50                                  55                                  60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
                   65                                  70                                  75                                  80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys

&lt;210&gt; 37

&lt;211&gt; 408

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(408)

&lt;400&gt; 37

atg gag ttt gga ctg agc tgg gtt ttc ctt gtc gct att ttc aaa ggt 48

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Phe Lys Gly

1

5

10

15

gtc cag tgt gaa gtg cag ttg gtg gag tct ggg gga ggc ttg gta cag 96

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln

20

25

30

ccg ggg ggg tcc ctg aga ctc gcc tgt gta ggc tct gga ttc gcc ttc 144

Pro Gly Gly Ser Leu Arg Leu Ala Cys Val Gly Ser Gly Phe Ala Phe

35

40

45

aga aac acc agg atg cac tgg att cga cag act cca gga aag agg ctg 192

Arg Asn Thr Arg Met His Trp Ile Arg Gln Thr Pro Gly Lys Arg Leu

50

55

60

gag tgg gtg gcc gac ata aag ttt gat gga agt gat ttt tac tat gta 240

Glu Trp Val Ala Asp Ile Lys Phe Asp Gly Ser Asp Phe Tyr Tyr Val

65

70

75

80

gac tct gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac 288

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn

85

90

95

tcc ctg tat ctg gaa atg aac agc ctg aga cct gat gac aca gcc gtc 336

64

aac cca ctc act tgg ggc cag gga gtc cag gtc acc gtc tcc tca 381  
Asn Pro Leu Thr Trp Gly Gln Gly Val Gln Val Thr Val Ser Ser  
115 120 125

 $\langle 222 \rangle \quad (1) \dots (417)$ 

ccc ggg gaa tct ctg agg atc tcc tgt aag act tct gga tac acc ttt 144

45

60

80

95

110

125

135

 $\langle 222 \rangle \quad (1) \dots (423)$



&lt;400&gt; 40

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct cct aga tgg 48  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

gtc ctg tcc cag gtg cag ttg cag gag tgc ggc cca gga gtg gtg aag 96  
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys  
 20 25 30

cct tgc gag acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc ttc 144  
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe  
 35 40 45

agt act tac tac tgg aat tgg atc cgc cag ccc cca ggg aag gga ctg 192  
 Ser Thr Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu  
 50 55 60

gag tgg att gga tat atc ggt ggt ggt ggt ggt cgc ccc aac tac aat 240  
 Glu Trp Ile Gly Tyr Ile Gly Gly Gly Gly Gly Arg Pro Asn Tyr Asn  
 65 70 75 80

tcc tcc ctc aag agt cgc atc acc ctg tca cta gac gcg tcc aag aac 288  
 Ser Ser Leu Lys Ser Arg Ile Thr Leu Ser Leu Asp Ala Ser Lys Asn  
 85 90 95

cag ttc tcc ctg aac ctg agc tct gtg acc gcc gcg gac acg gcc gtg 336  
 Gln Phe Ser Leu Asn Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 100 105 110

tac tac tgt gcc aga gat cgg ggc tac ggt gcc agc aat gat gct ttt 384  
 Tyr Tyr Cys Ala Arg Asp Arg Gly Tyr Gly Ala Ser Asn Asp Ala Phe  
 115 120 125

gat ttc tgg ggc caa ggg ctc agg gtc acc gtc tct tca 423  
 Asp Phe Trp Gly Gln Gly Leu Arg Val Thr Val Ser Ser  
 130 135 140

<213> Macaca cynomolgus

 $\langle 222 \rangle \quad (1) \dots (411)$ 

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca act cct aaa tgg 48  
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Thr Pro Lys Trp  
1 5 10 15

gtc ctg tcc cag gtg cag ttg cat gag tcg ggc cct gga ctg ctg aag 96  
Val Leu Ser Gln Val Gln Leu His Glu Ser Gly Pro Gly Leu Leu Lys  
20 25 30

cct tcg gag acc ctg tcc ctc acc tgc aat gtc tcc ggt gac tcc ccc 144  
Pro Ser Glu Thr Leu Ser Leu Thr Cys Asn Val Ser Gly Asp Ser Pro  
35 40 45

act aag tcc acg tgg aac tgg gtc cgc cag tcc cca ggg aag cca ctg 192  
Thr Lys Ser Thr Trp Asn Trp Val Arg Gln Ser Pro Gly Lys Pro Leu  
50 55 60

gaa tgg att ggt cat gtc ggt tct ggt gga ggt ggc ccc gtt tac aac 240  
Glu Trp Ile Gly His Val Gly Ser Gly Gly Gly Gly Pro Val Tyr Asn  
65 70 75 80

gtc ttc ttg acg ggt cgc gtc tcc atg tct cta gac gct tca aag aag 288  
Val Phe Leu Thr Gly Arg Val Ser Met Ser Leu Asp Ala Ser Lys Lys  
85 90 95

ctt ctc tcc ctg gcc tta gca tct gtg acc gcc gcc gac tcg gcc gtc 336  
Leu Leu Ser Leu Ala Leu Ala Ser Val Thr Ala Ala Asp Ser Ala Val

100

105

110

tat tac tgt gtc aga tcg acg gca tta ttt tcg ttg gat gtc tgg ggc  
Tyr Tyr Cys Val Arg Ser Thr Ala Leu Phe Ser Leu Asp Val Trp Gly

384

115

120

125

cgg gga ctt ctg gtc acc gtc tcc tca  
Arg Gly Leu Leu Val Thr Val Ser Ser

411

130

135

&lt;210&gt; 42

&lt;211&gt; 442

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(441)

&lt;400&gt; 42

atg gag ttg gga ctg agc tgg gtt ttc ctt ctt gtt gct att tta aaa  
Met Glu Leu Gly Leu Ser Trp Val Phe Leu Leu Val Ala Ile Leu Lys

48

1

5

10

15

ggc gtc cag tgt gac aag cag ctg gtg cag tcg ggg gga ggc ttg gtc  
Gly Val Gln Cys Asp Lys Gln Leu Val Gln Ser Gly Gly Gly Leu Val

96

20

25

30

cag cct ggc ggg tct ctg aga ctc gcc tgt gta gcc tcc gga ttc ccc  
Gln Pro Gly Gly Ser Leu Arg Leu Ala Cys Val Ala Ser Gly Phe Pro

144

35

40

45

ttc agt gac tat tac atg agt tgg gtc cgc cag gct cca ggg aag ggg  
Phe Ser Asp Tyr Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly

192

50

55

60

ttc cgc ttc a 442  
Phe Arg Phe  
145

1	5	10	15	
gtc ctg tcc cag gtg cag ttg gag gag tcg ggc cca gga ctg gtg aag				96
Val Leu Ser Gln Val Gln Leu Glu Glu Ser Gly Pro Gly Leu Val Lys				
20		25	30	
ccc tcg gag acc ctg tcc ctc acc tgc gct gtg tct ggt ggc ctc att				144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Leu Ile				
35		40	45	
act gga aac tac tgg aac tgg ctc cgg cag tca gaa ggg aag gga ctg				192
Thr Gly Asn Tyr Trp Asn Trp Leu Arg Gln Ser Glu Gly Lys Gly Leu				
50		55	60	
gag tgg att ggc cat att ggt ggt agt agt ggg aac acc ggc tac aac				240
Glu Trp Ile Gly His Ile Gly Gly Ser Ser Gly Asn Thr Gly Tyr Asn				
65		70	75	80
tcc gct ttc gag agt cgc gtc acc ttg tca aga gac acg gcc aag aat				288
Ser Ala Phe Glu Ser Arg Val Thr Leu Ser Arg Asp Thr Ala Lys Asn				
85		90	95	
cgg ttc tcc ctg aaa ctg acc tct gtg acc gcc gca gat tcg gcc gtc				336
Arg Phe Ser Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Ser Ala Val				
100		105	110	
tat tac tgt gcg aga tcg ggt ttt acc ggc acc gac ttc ttt tac tat				384
Tyr Tyr Cys Ala Arg Ser Gly Phe Thr Gly Thr Asp Phe Phe Tyr Tyr				
115		120	125	
tgg ggc ccg ggg aag tct tgg tc				407
Trp Gly Pro Gly Lys Ser Trp				
130		135		

&lt;210&gt; 44

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(420)

&lt;400&gt; 44

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg 48

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

1 5 10 15

gtc ctg tcc cag gtt caa cta cag gag tcg ggc cca gga ctg atg aag 96

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Met Lys

20 25 30

cct tcg gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tcc atc 144

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile

35 40 45

agc ggt ggt ttt ggc tgg ggc tgg atc cgt cag tcc ccg ggg aag ggg 192

Ser Gly Gly Phe Gly Trp Gly Trp Ile Arg Gln Ser Pro Gly Lys Gly

50 55 60

ctg gaa tgg att gga agt ttc tat act act act gga aat acc ttc tcc 240

Leu Glu Trp Ile Gly Ser Phe Tyr Thr Thr Thr Gly Asn Thr Phe Ser

65 70 75 80

aac ccc tcc ctc aag agt cga gtc acc att tca gcg gac acg tcc aag 288

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ala Asp Thr Ser Lys

85 90 95

aac cag ttc tcc ctg aga ctg acc tct gtg acc gcc gcg gac acg gcc 336

Asn Gln Phe Ser Leu Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala

100 105 110

gtt tat tac tgt gcg aga gat ctc tat agc agc ggc tat aaa ttt tac 384

Val Tyr Tyr Cys Ala Arg Asp Leu Tyr Ser Ser Gly Tyr Lys Phe Tyr  
 115 120 125

tac tgg ggc cag gga gtc ctg gtc acc gtc tcc tca 420

Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
 130 135 140

<210> 45

<211> 98

<212> PRT

<213> Macaca cynomolgus

<220>

<221> DOMAIN

<222> (31)...(35)

<223> CDRI

<221> DOMAIN

<222> (50)...(66)

<223> CDRII

<400> 45

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ala Cys Val Gly Ser Gly Phe Ala Phe Arg Asn Thr  
 20 25 30

Arg Met His Trp Ile Arg Gln Thr Pro Gly Lys Arg Leu Glu Trp Val  
 35 40 45

Ala Asp Ile Lys Phe Asp Gly Ser Asp Phe Tyr Tyr Val Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Glu Met Asn Ser Leu Arg Pro Asp Asp Thr Ala Val Tyr Phe Cys  
 85 90 95

Val Arg

<210> 46  
 <211> 98  
 <212> PRT  
 <213> Macaca cynomolgus

<220>  
 <221> DOMAIN  
 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 46

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Thr Thr Val  
 20 25 30  
 Phe Trp Ser Trp Leu Arg Gln Ser Pro Gly Ile Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Asn Phe Ala Gly Ser Thr Pro Glu Thr Asn Tyr Asn Pro Ser Leu  
 50 55 60  
 Lys Asn Arg Ala Thr Ile Ser Lys Asp Thr Pro Thr Asn Gln Phe Phe  
 65 70 75 80  
 Leu Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys  
 85 90 95  
 Ala Arg

<210> 47  
 <211> 98  
 <212> PRT  
 <213> Macaca cynomolgus

<220>



&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 47

Glu Val His Leu Val Gln Ser Gly Ala Gln Val Lys Arg Pro Gly Glu

1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Asp Ser

20 25 30

Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met

35 40 45

Gly Asn Ile Tyr Pro Gly Asp Ser Asp Ser Arg Tyr Asn Pro Ser Phe

50 55 60

Gln Gly Arg Val Thr Ile Ser Val Asp Lys Ser Ile Ser Thr Thr Tyr

65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Thr Tyr Tyr Cys

85 90 95

Ala Lys

&lt;210&gt; 48

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

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<210> 49
<211> 98
<212> PRT
<213> Macaca cynomolgus
<220>
<221> DOMAIN
<222> (31) ... (35)
<223> CDRI
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Gln	Val	Gln	Leu	His	Glu	Ser	Gly	Pro	Gly	Leu	Leu	Lys	Pro	Ser	Glu
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Asn	Val	Ser	Gly	Asp	Ser	Pro	Thr	Lys	Ser
			20					25					30		
Thr	Trp	Asn	Trp	Val	Arg	Gln	Ser	Pro	Gly	Lys	Pro	Leu	Glu	Trp	Ile

35 40 45  
 Gly His Val Gly Ser Gly Gly Gly Gly Pro Val Tyr Asn Val Phe Leu  
 50 55 60  
 Thr Gly Arg Val Ser Met Ser Leu Asp Ala Ser Lys Lys Leu Leu Ser  
 65 70 75 80  
 Leu Ala Leu Ala Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys  
 85 90 95  
 Val Arg

<210> 50  
 <211> 100  
 <212> PRT  
 <213> Macaca cynomolgus

<220>  
 <221> DOMAIN  
 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(68)  
 <223> CDRII

<400> 50

Asp Lys Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ala Cys Val Ala Ser Gly Phe Pro Phe Ser Asp Tyr  
 20 25 30  
 Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu  
 35 40 45  
 Gly Leu Ile Lys Thr Asn Pro Asp Gly Gly Thr Thr Asp Tyr Ala Ala  
 50 55 60  
 Ser Val Lys Gly Arg Phe Ile Ile Ser Arg Asp Asp Ser Lys Asn Ser  
 65 70 75 80  
 Leu Phe Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr  
 85 90 95

Tyr Cys Thr Thr

100

&lt;210&gt; 51

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 51

Gln Val Gln Leu Glu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Leu Ile Thr Gly Asn

20 25 30

Tyr Trp Asn Trp Leu Arg Gln Ser Glu Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly His Ile Gly Gly Ser Ser Gly Asn Thr Gly Tyr Asn Ser Ala Phe

50 55 60

Glu Ser Arg Val Thr Leu Ser Arg Asp Thr Ala Lys Asn Arg Phe Ser

65 70 75 80

Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys

85 90 95

Ala Arg

&lt;210&gt; 52

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(36)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (51)...(67)

&lt;223&gt; CDRII

&lt;400&gt; 52

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Met Lys Pro Ser Glu  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Gly Gly  
 20 25 30  
 Phe Gly Trp Gly Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp  
 35 40 45  
 Ile Gly Ser Phe Tyr Thr Thr Thr Gly Asn Thr Phe Ser Asn Pro Ser  
 50 55 60  
 Leu Lys Ser Arg Val Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe  
 65 70 75 80  
 Ser Leu Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
 85 90 95  
 Cys Ala Arg

&lt;210&gt; 53

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(390)

&lt;400&gt; 53

atg gac ata agg gtc ccc gtg cag ctc ctg ggg ctc ctg ttg ctc tgg

48

Met Asp Ile Arg Val Pro Val Gln Leu Leu Gly Leu Leu Leu Leu Trp

1 5 10 15

ctc cga ggt gcc aga tgt gac atc cag atg acc cag tct cca tcc tcc 96

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser

20 25 30

ctg tct aca tct gta gga gac act gtc acc atc act tgc cgg gcg agt 144

Leu Ser Thr Ser Val Gly Asp Thr Val Thr Ile Thr Cys Arg Ala Ser

35 40 45

caa ggc att gac acg gag tta gcc tgg tat cag cag aaa cca ggt aaa 192

Gln Gly Ile Asp Thr Glu Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys

50 55 60

gcc ccc aca ctc ctg atc tct gat gcc tcc agg ttg cag acg ggg gtc 240

Ala Pro Thr Leu Leu Ile Ser Asp Ala Ser Arg Leu Gln Thr Gly Val

65 70 75 80

tca tct cgg ttc agc ggc agt gga tct gga aca gat ttc act ctc acc 288

Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

85 90 95

atc aac agc ctg cag cct gaa gat att gcg act tat tac tgt caa cag 336

Ile Asn Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln

100 105 110

gat aat agt ttt cca ctc act ttc ggc gga ggg acc aag gtg gag atc 384

Asp Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile

115 120 125

aaa cga 390

Lys Arg

130

<210> 54

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(384)

&lt;400&gt; 54

gtc ttc att tcc ctg ttg ctc tgg atc tct ggt gcc tgt ggg gac att 48  
 Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Cys Gly Asp Ile  
 1 5 10 15

gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg gga gag agg 96  
 Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg  
 20 25 30

gtc acc atc aat tgt aag tcc agc cag agt ctt tta tac agc tcc aac 144  
 Val Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn  
 35 40 45

aat aag aac tac tta gcc tgg tac cag caa aaa cca gga cag gct cct 192  
 Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro  
 50 55 60

caa cta ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc cct aat 240  
 Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asn  
 65 70 75 80

cga ttt agt ggc agc ggc tct ggg aca gat ttc act ctc acc atc agt 288  
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
 85 90 95

ggc ctg cag gct gaa gat gtg gca gtg tat tac tgt caa cag tat tat 336  
 Gly Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr  
 100 105 110

gat atg ccc gac agt ttt ggc cag ggg acc aaa gtg gac atc aaa cga 384  
 Asp Met Pro Asp Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg  
 115 120 125

<210> 55

<211> 399

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1)...(399)

<400> 55

atg agg ctc cct gct cag ctc ctg ggg ctg cta ttg ctc tgc gtc ccc 48  
 Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys Val Pro  
 1 5 10 15

gga tcc agt ggg gat gtt gtg atg act cag tct cca ctc tcc ctg ccc 96  
 Gly Ser Ser Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro  
 20 25 30

gtc atc cct gga cag cca gcc tcc atc tcc tgc agg tct agt caa agc 144  
 Val Ile Pro Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser  
 35 40 45

ctt gta cat agt gac ggg aaa acc tac ttg aat tgg tta caa cag aag 192  
 Leu Val His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Lys  
 50 55 60

cca ggc caa cct cca aga ctc ctg att tat cag gtt tct aac cgg cac 240  
 Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Gln Val Ser Asn Arg His  
 65 70 75 80

tct ggg gtc cca gac aga ttc agc ggc agt ggg gca ggg aca gac ttc 288  
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe



85

90

95

aca ctg aaa atc agc aga gtg gag act gag gat gtt ggg gtt tat tcc 336  
 Thr Leu Lys Ile Ser Arg Val Glu Thr Glu Asp Val Gly Val Tyr Ser

100

105

110

tgc gtg caa ggt aca cac tgg ccg tgg acg ttc ggc caa ggg acc aag 384  
 Cys Val Gln Gly Thr His Trp Pro Trp Thr Phe Gly Gln Gly Thr Lys

115

120

125

gtg gac atc aaa cga 399

Val Asp Ile Lys Arg

130

&lt;210&gt; 56

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(384)

&lt;400&gt; 56

atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc cca 48  
 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro

1

5

10

15

ggt gcc ata tgt gac att cag atg tcc cag tct cca tcc tcc ctg tct 96  
 Gly Ala Ile Cys Asp Ile Gln Met Ser Gln Ser Pro Ser Ser Leu Ser

20

25

30

gct tct gtg gga gac aga gtc acc atc acc tgc cgg gca agt cag ggc 144  
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly

35

40

45

ata act aat tat tta aac tgg tat cag cag aaa ccg ggg aaa gcc cct 192  
 ile thr asn tyr leu asn trp tyr gln gln lys pro gly lys ala pro  
 50 55 60

aac ctg ctg atc tat tat gca act cgt ttg ggc agc ggg gtc cca tca 240  
 asn leu leu ile tyr tyr ala thr arg leu ala ser gly val pro ser  
 65 70 75 80

agg ttc agc ggc agt gga tct ggg tcg gag tac agt ctg gcc atc agc 288  
 arg phe ser gly ser gly ser gly ser glu tyr ser leu ala ile ser  
 85 90 95

agc ctg cag cct gaa gat ttt gca acc tat ttc tgt caa cag ggt tat 336  
 ser leu gln pro glu asp phe ala thr tyr phe cys gln gln gly tyr  
 100 105 110

agg gcc ccc tac act ttt ggc cag ggg acc aca gtg gag atc aaa cga 384  
 arg ala pro tyr thr phe gly gln gly thr thr val glu ile lys arg  
 115 120 125

<210> 57

<211> 390

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1)...(390)

<400> 57

atg gac atg agg gtc ccc gct cag ctg ctg ggg ctg ctg ctg tgg 48  
 met asp met arg val pro ala gln leu leu gly leu leu leu leu trp  
 1 5 10 15

ctc cta ggt gcc aga tgt gac atc cag atg acc cag tct cct tct tcc 96  
 leu leu gly ala arg cys asp ile gln met thr gln ser pro ser ser

20

25

30

ttg tct gca tct gta gga gac aga gtc acc atc act tgc caa gcc agt 144  
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser

35

40

45

cag ggt att agc aac tgg tta gcc tgg tat cag cag aaa ccg ggg aaa 192  
 Gln Gly Ile Ser Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys

50

55

60

gcc cct aag ctc ctg atc tat gct gca tcc act ttc caa agt ggg gtc 240  
 Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Phe Gln Ser Gly Val

65

70

75

80

cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc 288  
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr

85

90

95

atc agc agc ctg cag cct gaa gat ttt gca act tac tac tgt caa cag 336  
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln

100

105

110

tat aat act tac cct ctc act ttc ggc gga ggg acc aag gtg gag atc 384  
 Tyr Asn Thr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile

115

120

125

aaa cga 390

Lys Arg

130

<210> 58

<211> 390

<212> DNA

<213> Macaca cynomolgus

<220>

&lt;221&gt; CDS

&lt;222&gt; (1)...(390)

&lt;400&gt; 58

atg gac ttg agg gcc ccc gct cat ctc cta ggg ctc ctg ctg ctc tgg	48
Met Asp Leu Arg Ala Pro Ala His Leu Leu Gly Leu Leu Leu Leu Trp	
1 5 10 15	
ctc cca ggt gcc aga ggt gac atc cag atg acc cag tct cca ccc tcc	96
Leu Pro Gly Ala Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Pro Ser	
20 25 30	
ctg tct gcg tct gtt ggg gac act gtc agt ctt act tgt cgg gca agt	144
Leu Ser Ala Ser Val Gly Asp Thr Val Ser Leu Thr Cys Arg Ala Ser	
35 40 45	
cag cct att ggc agt aat tta aat tgg ttc cag caa aaa cct ggg agc	192
Gln Pro Ile Gly Ser Asn Leu Asn Trp Phe Gln Gln Lys Pro Gly Ser	
50 55 60	
ccc ccc aga ctc ctg atc tac ctt gcg acc gcc ttg caa cgt ggg atc	240
Pro Pro Arg Leu Leu Ile Tyr Leu Ala Thr Ala Leu Gln Arg Gly Ile	
65 70 75 80	
ccg tca agg ttt agc gcc act gga tct caa acc aat ttc act ctc acg	288
Pro Ser Arg Phe Ser Ala Thr Gly Ser Gln Thr Asn Phe Thr Leu Thr	
85 90 95	
atc acc ggc ctg cag cct gag gat ttc gca act tac ctc tgt ctg caa	336
Ile Thr Gly Leu Gln Pro Glu Asp Phe Ala Thr Tyr Leu Cys Leu Gln	
100 105 110	
cat act tct tac cca ttc act ttt ggc ccc ggg aca aag gtg gat atc	384
His Thr Ser Tyr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile	
115 120 125	
aag cga	390

Lys Arg

130

&lt;210&gt; 59

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(56)

&lt;223&gt; CDRII

&lt;400&gt; 59

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Thr Ser Val Gly

1 5 10 15

Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Asp Thr Glu

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Thr Leu Leu Ile

35 40 45

Ser Asp Ala Ser Arg Leu Gln Thr Gly Val Ser Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro

65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys

85

&lt;210&gt; 60

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(40)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (56)...(62)

&lt;223&gt; CDRII

&lt;400&gt; 60

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly

1 5 10 15

Glu Arg Val Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser

20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

35 40 45

Ala Pro Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val

50 55 60

Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

65 70 75 80

Ile Ser Gly Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys

85 90

&lt;210&gt; 61

&lt;211&gt; 93

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(39)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (54)...(61)

&lt;223&gt; CDRII

89

Ser Gly Ser Gly Ser Glu Tyr Ser Leu Ala Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Phe Cys  
 85

<210> 63  
 <211> 88  
 <212> PRT  
 <213> Macaca cynomolgus

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(56)  
 <223> CDRII

<400> 63

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Gly Ile Ser Asn Trp  
 20 25 30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Ala Ala Ser Thr Phe Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys  
 85

<210> 64  
 <211> 88  
 <212> PRT  
 <213> Macaca cynomolgus



&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(56)

&lt;223&gt; CDRII

&lt;400&gt; 64

Asp Ile Gln Met Thr Gln Ser Pro Pro Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Thr Val Ser Leu Thr Cys Arg Ala Ser Gln Pro Ile Gly Ser Asn  
 20 25 30  
 Leu Asn Trp Phe Gln Gln Lys Pro Gly Ser Pro Pro Arg Leu Leu Ile  
 35 40 45  
 Tyr Leu Ala Thr Ala Leu Gln Arg Gly Ile Pro Ser Arg Phe Ser Ala  
 50 55 60  
 Thr Gly Ser Gln Thr Asn Phe Thr Leu Thr Ile Thr Gly Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Leu Cys  
 85

&lt;210&gt; 65

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(360)

&lt;400&gt; 65

gac acg gtg ctg acc cag tct cct gct ttg gct gtg cct cca gga gag  
 Asp Thr Val Leu Thr Gln Ser Pro Ala Leu Ala Val Pro Pro Gly Glu  
 1 5 10 15

48

agg gtt acc gtc tcc tgt agg gcc agt gaa agt gtc agt aca ttt ttg 96  
 Arg Val Thr Val Ser Cys Arg Ala Ser Glu Ser Val Ser Thr Phe Leu  
 20 25 30

cac tgg tat caa cag aaa cca gga cat caa ccc aaa ctc ctc atc tat 144  
 His Trp Tyr Gln Gln Lys Pro Gly His Gln Pro Lys Leu Leu Ile Tyr  
 35 40 45

cta gcc tca aaa cta gaa tct ggg gtc cct gcc agg ttc agt ggc ggt 192  
 Leu Ala Ser Lys Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Gly  
 50 55 60

ggg tct ggg aca gac ttc acc ctc acc att gat cct gtg gag gct gat 240  
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asp Pro Val Glu Ala Asp  
 65 70 75 80

gac act gct acc tat tac tgt cag cag acc tgg aat gat cct cgg acg 288  
 Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Thr Trp Asn Asp Pro Arg Thr  
 85 90 95

ttc ggt gga ggc acc aag ctg gaa ttg aaa cgg gct gat gct gca cca 336  
 Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro  
 100 105 110

act gta tct atc ttc cca cca tcc 360  
 Thr Val Ser Ile Phe Pro Pro Ser  
 115 120

<210> 66

<211> 360

<212> DNA

<213> Rat

<220>

<221> CDS

&lt;222&gt; (1)...(360)

&lt;400&gt; 66

gag gtc cag ctg cag cag tct gga cct gag gtt ggg agg cct ggg tcc 48

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Val Gly Arg Pro Gly Ser

1 5 10 15

tca gtc aag att tct tgc aag gct tct ggc tac acc ttt aca gat tac 96

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr

20 25 30

gtt ttg aat tgg gtg aag cag agt cct gga cag gga ctg gaa tgg ata 144

Val Leu Asn Trp Val Lys Gln Ser Pro Gly Gln Gly Leu Glu Trp Ile

35 40 45

gga tgg att gat cct gac tat ggt act act gat tat gct gag aag ttc 192

Gly Trp Ile Asp Pro Asp Tyr Gly Thr Thr Asp Tyr Ala Glu Lys Phe

50 55 60

aaa aag aag gcc aca ctg act gca gat aca tcc tcc agc aca gcc tac 240

Lys Lys Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65 70 75 80

atc cag ctt agc agc ctg aca tct gag gac aca gcc acc tat ttt tgt 288

Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Thr Tyr Phe Cys

85 90 95

gct aga tct agg aat tac gga gga tat att aat tac tgg ggc caa gga 336

Ala Arg Ser Arg Asn Tyr Gly Gly Tyr Ile Asn Tyr Trp Gly Gln Gly

100 105 110

gtc atg gtc aca gtc tcc tca gct 360

Val Met Val Thr Val Ser Ser Ala

115 120

&lt;210&gt; 67

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 67

Ala Val His Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Ser Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Asn Ile Tyr  
 20 25 30  
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Phe Asp Ala Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Arg Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Cys Gly Trp Gly Thr His Pro  
 85 90 95  
 Tyr Asn Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
 100 105

&lt;210&gt; 68

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; rat/chimpanzee sequence

&lt;400&gt; 68

Asp Thr Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Ser Val Thr Ile Thr Cys Arg Ala Ser Glu Ser Val Ser Thr Phe  
 20 25 30  
 Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Leu Ala Ser Lys Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly  
 50 55 60

95

&lt;400&gt; 70

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asp Tyr  
 20 25 30  
 Val Leu Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Trp Ile Asp Pro Asp Tyr Gly Thr Thr Asp Tyr Ala Glu Lys Phe  
 50 55 60  
 Lys Lys Lys Ala Thr Leu Ser Ala Asp Thr Ser Arg Asn Ser Ala Tyr  
 65 70 75 80  
 Leu Gln Met Asn Asp Leu Arg Pro Glu Asp Thr Ala Ile Tyr Phe Cys  
 85 90 95  
 Ala Arg Ser Arg Asn Tyr Gly Gly Tyr Ile Asn Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser  
 115

&lt;210&gt; 71

&lt;211&gt; 354

&lt;212&gt; DNA

&lt;213&gt; Murine

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(354)

&lt;400&gt; 71

caa gtt cag ctt caa cag tct gga gct gag ctg atg aag cct ggg gcc 48  
 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala  
 1 5 10 15  
 tca gtg aag ata tcc tgc aag gct act ggc tac aca ttc agt agc tac 96  
 Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr  
 20 25 30

tgg ata gag tgg gta aag cag agg cct gga cat ggc ctt gag tgg att 144  
 Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile  
           35                          40                          45

gga gag att tta cct aga agt ggt aat act aac tac aat gag aag ttc 192  
 Gly Glu Ile Leu Pro Arg Ser Gly Asn Thr Asn Tyr Asn Glu Lys Phe  
           50                          55                          60

aag ggc aag gcc aca ttc act gca gaa aca tcc tcc aac aca gcc tac 240  
 Lys Gly Lys Ala Thr Phe Thr Ala Glu Thr Ser Ser Asn Thr Ala Tyr  
           65                          70                          75                          80

atg caa ctc agc agc ctg aca cct gag gac tct gcc gtc tat tac tgt 288  
 Met Gln Leu Ser Ser Leu Thr Pro Glu Asp Ser Ala Val Tyr Tyr Cys  
                                   85                          90                          95

tca agt cgc ggc gtc agg ggc tct atg gac tac tgg ggt caa gga acc 336  
 Ser Ser Arg Gly Val Arg Gly Ser Met Asp Tyr Trp Gly Gln Gly Thr  
                           100                          105                          110

tca gtc acc gtc tcc tca 354  
 Ser Val Thr Val Ser Ser  
           115

<210> 72

<211> 324

<212> DNA

<213> Murine

<220>

<221> CDS

<222> (1)...(324)

<400> 72

gat att cag atg acc cag act aca tcc tcc ctg tct gcc tct ctg gga 48  
 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly

1	5	10	15	
gac aga gtc acc atc act tgc agg tca agt cag gac att agc aat ttt				96
Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Asp Ile Ser Asn Phe				
20		25	30	
tta aac tgg tat cag cag aaa cca gat gga act gtt aaa ctc ctg atc				144
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile				
35		40	45	
tac tac aca tca aca tta cac tca gga gtc cca tca agg ttc agt ggc				192
Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly				
50		55	60	
agt ggg tct gga aca gat tat tct ctc acc att agc aac ctg gag caa				240
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln				
65		70	75	80
gaa gat att gcc act tac ttt tgc caa cag ggt aat acg ctt cct tgg				288
Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp				
85		90	95	
acg ttc ggt gga ggc acc aac ctg gaa atc aaa cgg				324
Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys Arg				
100		105		

&lt;210&gt; 73

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; murine/chimpanzee sequence

&lt;400&gt; 73

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly



1                    5                    10                    15  
 Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Asp Ile Ser Asn Phe  
                   20                    25                    30  
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
                   35                    40                    45  
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly  
                   50                    55                    60  
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65                    70                    75                    80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp  
                   85                    90                    95  
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
                   100                    105

<210> 74

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> murine/chimpanzee sequence

<400> 74

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1                    5                    10                    15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr  
                   20                    25                    30  
 Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
                   35                    40                    45  
 Gly Glu Ile Leu Pro Arg Ser Gly Asn Thr Asn Tyr Asn Glu Lys Phe  
                   50                    55                    60  
 Lys Gly Lys Ala Ser Phe Asn Ala Asp Thr Ser Thr Asn Ile Ala Tyr  
 65                    70                    75                    80  
 Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                    90                    95  
 Ser Ser Arg Gly Val Arg Gly Ser Met Asp Tyr Trp Gly Gln Gly Thr  
                   100                    105                    110

Leu Val Thr Val Ser Ser

115

&lt;210&gt; 75

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Murine

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(360)

&lt;400&gt; 75

caa gtt cag ctt caa cag cct ggg gct gag ctt gtg aag tct ggg gcc 48

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Ser Gly Ala

1 5 10 15

tca gtg aag ctg tcc tgc aag gct tct ggc agt acc ttc acc agc tac 96

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Ser Thr Phe Thr Ser Tyr

20 25 30

tgg atg cac tgg gtg aag cag agg cct gga cga ggc ctt gag tgg att 144

Trp Met His Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile

35 40 45

gga agg att gat cca aat agt ggt ggt act aag gat aat gag aag ttc 192

Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Asp Asn Glu Lys Phe

50 55 60

aag agc aag gcc aca ctg act gta gac aaa ccc tcc agc aca gcc tac 240

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Pro Ser Ser Thr Ala Tyr

65 70 75 80

atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc tat tat tgt 288

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys

85 90 95

gca aga gag acc tac tat gat tcc tcg ttt gct tac tgg ggc caa ggg 336  
 Ala Arg Glu Thr Tyr Tyr Asp Ser Ser Phe Ala Tyr Trp Gly Gln Gly  
 100 105 110

act ctg gtc act gtc tct gca gcc 360  
 Thr Leu Val Thr Val Ser Ala Ala  
 115 120

<210> 76

<211> 336

<212> DNA

<213> Murine

<220>

<221> CDS

<222> (1)...(336)

<400> 76

gat att gtt atg act cag tct caa aaa ttc atg tcc aca tca gta gga 48  
 Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly  
 1 5 10 15

gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg ggt act aat 96  
 Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30

gta gcc tgg tat caa cag aaa cca ggg caa tct cct aaa gca ctg att 144  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile  
 35 40 45

tac tcg gca tcc tac cgg tac agt gga gtc cct gat cgc ttc aca ggc 192  
 Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly  
 50 55 60

agt gga tct ggg aca gat ttc act ctc acc atc agc aat gtg cag tct 240  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser

80

acg ttc ggt gct ggg acc aag ctg gag ctg aaa cgg gct gat gct gca 336  
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala  
100 105 110

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<210> 77
<211> 107
<212> PRT
<213> Artificial Sequence
<220>
<223> murine/chimpanzee sequence
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<400> 77

Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asn	Val	Gly	Thr	Asn
			20					25					30		
Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Ala	Leu	Ile
		35					40					45			
Tyr	Ser	Ala	Ser	Tyr	Arg	Tyr	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Ser	Tyr	Pro	Leu
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
				100					105						

<210> 78  
<211> 118

<213> Artificial Sequence

<223> murine/chimpanzee sequence

[illegible]

<211> 119

<213> Artificial Sequence

<223> murine/human sequence

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Ser Thr Phe Thr Ser Tyr  
20 25 30

Trp Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Asp Asn Glu Lys Phe  
 50 55 60  
 Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Glu Thr Tyr Tyr Asp Ser Ser Phe Ala Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Met Val Thr Val Ser Ala  
 115

<210> 80

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> murine/human sequence

<400> 80

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
 35 40 45  
 Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu  
 85 90 95  
 Thr Phe Gly Gly Gly Thr  
 100

&lt;210&gt; 81

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 81

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 82

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 82

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 83

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 83

Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 84

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 84

Trp Gly Gln Gly Ile Leu Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 85

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 85

Trp Gly Arg Gly Ile Leu Val Ile Val Ser Ser

1

5

10

&lt;210&gt; 86

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 86

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg

1

5

10

&lt;210&gt; 87

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 87

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg

1

5

10

&lt;210&gt; 88

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 88

Trp Gly Arg Gly Val Leu Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 89

&lt;211&gt; 11



&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 89

Trp Gly Gln Gly Val Gln Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 90

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 90

Trp Gly Pro Gly Val Met Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 91

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 91

Trp Gly Arg Gly Leu Leu Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 92

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 92

Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 93

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 93

Trp Gly Gln Gly Leu Arg Val Thr Val Ser Ser

1 5 10

&lt;210&gt; 94

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 94

Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg

1 5 10

&lt;210&gt; 95

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 95

Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg

1 5 10

&lt;210&gt; 96

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 96

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg

1 5 10

&lt;210&gt; 97

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

<400> 97

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg

1

5

10

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